Inherited STING-activating mutation underlies a familial inflammatory syndrome with lupus-like manifestations

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Innate immunity to viral infection involves induction of the type I IFN response; however, dysfunctional regulation of this pathway leads to inappropriate inflammation. Here, we evaluated a nonconsanguineous family of mixed European descent, with 4 members affected by systemic inflammatory and autoimmune conditions, including lupus, with variable clinical expression. We identified a germline dominant gain-of-function mutation in TMEM173, which encodes stimulator of type I IFN gene (STING), in the affected individuals. STING is a key signaling molecule in cytosolic DNA-sensing pathways, and STING activation normally requires dimerization, which is induced by 2′-3′ cyclic GMP-AMP (cGAMP) produced by the cGAMP synthase in response to cytosolic DNA. Structural modeling supported constitutive activation of the mutant STING protein based on stabilized dimerization. In agreement with the model predictions, we found that the STING mutant spontaneously localizes in the Golgi of patient fibroblasts and is constitutively active in the absence of exogenous 2′-3′-cGAMP in vitro. Accordingly, we observed elevated serum IFN activity and a type I IFN signature in peripheral blood from affected family members. These findings highlight the key role of STING in activating both the innate and adaptive immune responses and implicate aberrant STING activation in features of human lupus.

Introduction

The type I IFN response is a key component of innate immunity to viral infection. A tight control of this pathway is required to avoid disease-causing inflammation. This is well illustrated by the elucidation of the genetic basis of Aicardi-Goutières syndrome (AGS), an inflammatory phenotype sometimes mimicking pathogenic viral infection, which is related to enhanced type I IFN signaling as a consequence of mutations in TREX1, RNASEH2A, RNASEH2B, RNASEH2C, SAMHD1, and ADAR (1–4). All of these proteins normally participate in regulating nucleic acid metabolism, and their dysfunction leads to an accumulation in the cytosol of nucleic acid, which is then detected to instigate a prototypic antiviral response. Recently, gain-of-function mutations in IFIHI1 (also known as MDA-5), encoding a cytosolic viral RNA receptor, were reported in patients demonstrating a spectrum of inflammatory phenotypes, including classical AGS (5). Similarly, cytosolic DNA sensors have been described as leading to type I IFN and inflammatory cytokine induction (e.g., IL-1 and IL-18) (6, 7). In particular, stimulator of type I IFN gene (STING) has been identified as a central mediator of responses to cytosolic DNA upon induced dimerization (8–11) and as the receptor of 2′-3′ cyclic GMP-AMP (cGAMP) produced by the recently described DNA sensor cGAMP synthase (12, 13). In this report, we describe an inherited dominant TMEM173 mutation leading to constitutive activation of STING and thereby to an inflammatory and a lupus-like disease.

Results and Discussion

Clinical presentation and familial history. We report 4 members of a single kindred (Figure 1, A and B) exhibiting a complex systemic inflammatory syndrome associated with pulmonary fibrosis (Figure 1, B and C) and autoimmunity (Table 1, Supplemental Methods, and Supplemental Table 1; supplemental material available online with this article; doi:10.1172/JCI79100DS1). The index case had early-onset febrile attacks, malar rash, lung disease, and failure to thrive. The clinical history suggested a familial syndrome, with variable clinical expression. The proband’s father (II-5) and paternal uncle (II-6) are monozygotic twins and presented with a sim-
is located in the first highly hydrophobic helix (α5) of the CTD of STING that forms intermolecular hydrophobic interactions also involving helix α7 (Supplemental Figure 1). Within the dimer, p.V155 is at the center of a hydrophobic network, in the vicinity of the closest contact between the 2 subunits (p.G158) (Supplemental Figure 1B). This network is similar whatever the conformational state of the protein (bound or not to cyclic dinucleotides). There is only one major possibility for accommodating the methionine side chain of the p.V155M substitution (Supplemental Figure 1C), which is predicted to lead to the establishment of a strikingly tighter network of interactions. The p.V155M substitution is likely to stabilize the position of p.M271 from the same subunit, which forms a strong sulfur-aromatic interaction with p.W161 from the other subunit. This should reinforce the stability of the dimer. It is thus possible that the p.V155M mutant mimics the effect of ligand binding.

Constitutive activation of the V155M mutant in vitro. To examine the activity of the p.V155M mutated STING protein, we used a luciferase reporter assay that includes the IFN-β gene promoter. In this assay, overexpression of wild-type STING protein activated the IFNB promoter 2-fold over control in the absence of ligand (Figure 2A). Stimulation with synthetic 2′3′-cGAMP enhanced promoter activation in a dose-dependent manner, and this induction was not observed in the absence of STING (Figure 2A). In contrast, the p.V155M mutant induced reporter activity in the absence of syn-
**Table 1. Clinical features of family members carrying V155M**

<table>
<thead>
<tr>
<th>Age of onset</th>
<th>I-4</th>
<th>II-5</th>
<th>II-6</th>
<th>III-2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gender</td>
<td>Male</td>
<td>Male</td>
<td>Male</td>
<td>Female</td>
</tr>
<tr>
<td>Age at last fu (yr)</td>
<td>65</td>
<td>29</td>
<td>33</td>
<td>4</td>
</tr>
<tr>
<td>Status at last fu</td>
<td>Alive</td>
<td>Died</td>
<td>Alive</td>
<td>Alive</td>
</tr>
</tbody>
</table>

Febrile attacks: - ; + ; + ; +
Failure to thrive: - ; + ; + ; +
Sparse and thin hair: - ; + ; + ; +
Relapsing malar rash: - ; + ; + ; +
Interstitial lung disease: - ; + ; + ; +
Lung biopsy: Not done | MA, FH, and IF | MA, FH, and IF | MA, FH, and IF
Arthralgia/arthritis: +; +; +; -
ESR: Elevated | Elevated | Elevated | Elevated
CRP: Elevated | Elevated | Elevated | Elevated
Native anti-DNA (IU/l): 40; 521; 1030; 512
Native anti-DNA (IU/l): 4.1–10.2

*AThe first test was negative; the second test was positive and resulted in the value shown. fu, follow-up; Neg, negative; MA, macrophage alveolitis; FH, follicular hyperplasia; IF, interstitial fibrosis; ESR, erythrocyte sedimentation rate; CRP, C-reactive protein; ANA, antinuclear antibody (n < 1:100); RF, rheumatoid factor (n < 20 IU/l). Native anti-DNA (n < 5.5 IU/l).*

**Figure 2. Constitutive activation of the mutant STING in vitro.** (A) Luciferase induction in HEK293FT cells cotransfected with empty vector (EV), wild-type STING, V155M STING, and a luciferase plasmid under the control of the IFNB promoter and stimulated with increasing amounts of synthetic 2′3′-cGAMP complexed to lipofectamine (maximal dose, 4 μg/ml; dose–response dilution factor, 3) (n = 3, mean and SEM; paired t test, *P < 0.05). (B) Immunoblot of STING expression in HEK293FT cells transfected with wild-type and V155M STING (representative of 3 independent experiments).

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fibroblasts (Figure 3A). Upon 2′3′-cGAMP activation, mutant STING remained localized to the Golgi and the perinuclear vesicles (Figure 3D), whereas wild-type STING was mostly observed in the latter structures (Figure 3B). These findings indicate that mutant STING is likely activated in vivo in patient cells independently of ligand addition and that there is only limited further activation following 2′3′-cGAMP stimulation.

**Functional consequences of the V155M STING mutant.** Activation of STING is known to induce type I IFN production through TBK-1 phosphorylation and IRF3 phosphorylation (9). In order to study the functional consequences of the V155M STING variant, we assessed the expression of 6 gene transcripts known to be overexpressed in PBMCs of patients with AGS (IFI44L, SIGLEC1, RSAD2, IFI27, IFIT1, and ISG15) (17). Positive controls were generated by treatment of healthy control PBMCs with IFN-α (1,000 U/ml) for 6 hours (18). PBMCs from the patient (III-2) and her grandfather (I-4) exhibited an overexpression of all 6 tested genes as compared with control PBMCs and PBMCs from the healthy mother (II-4) (Supplemental Figure 2). Similar overexpression was also seen in in vitro–activated T cells (Supplemental Figure 3). In contrast, a set of non–type I IFN–regulated genes remained normally expressed in peripheral blood compared with control samples (Supplemental Figure 4). These results suggest that cells with the V155M variant spontaneously express type I IFN. Accordingly, serum-type I IFN activity was found to be elevated in patient blood (III-2).

Collectively, the results reported here suggest a gain-of-function consequence of the V155M variant. The constitutively active mutant thus results in upregulated type I IFN production, as measured by serum IFN activity, and a type I IFN signature in whole blood. The very same mutation and 2 other mutations at neighboring residues have been recently reported to be associated with inflammation and severe vasculopathy in humans (19). The present work thus confirms the gain-of-function nature of the V155M mutation, provides a structural model accounting for constitutive mutant STING activity, and extends the spectrum of clinical phenotypic expression.
Our findings highlight the central role of STING in type I IFN production and demonstrate its causal role in inflammatory syndromes variably accompanied with small vessel vasculopathy, pulmonary fibrosis, and autoimmunity reminiscent of SLE. Hence, TMEM173 gain-of-function mutations should be screened for as a monogenic cause of this broad spectrum of diseases. STING could represent a new therapeutic target in these disorders as well as other more common inflammatory diseases triggered by cytosolic DNA stimulation of microbial or endogenous origin, resulting in dysregulated type I IFN production.

Methods
Further details are provided in the Supplemental Methods.

Statistics. Analyses were performed with PRISM software (version 4 for Macintosh, GraphPad Inc.). Statistical hypotheses were tested using 2-tailed t test. A P value of less than 0.05 was considered significant.

Study approval. Written informed consent (parental consent, in case of minors) was obtained from all participants of the study. The study and protocols conform to the 1975 Declaration of Helsinki and were approved by the comité de protection des personnes Ile de France II and the French advisory committee on data processing in medical research.

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